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1	AGCTCACAGCC	11
12	ATGGTTACCTTCAGCCACGTCTCCAGTCTGAGTCACTGGTTCCTCTTGCTGCTGCTGCTG	71
1	<u>M V T F S H V S S L S H W F L L L L L L</u>	20
72	AATCTGTTCTTGCCGGTAATATTTGCTATGCCTGAATCATACTCCTTCAACTGTCCCGAT	131
21	<u>N L F L P V I F A M P E S Y S F N C P D</u>	40
132	GGTGAATACCAGTCTAATGATGTCTGTTGCAAGACCTGTCCCTCAGGTACATTTGTCAAG	191
41	G E Y Q S N D V C C K T C P S G T F V K	60
192	GCGCCCTGCAAAATCCCCATACTCAAGGACAATGTGAGAAGTGTACCCAGGAACATTC	251
61	A P C K I P H T Q G Q C E K C H P G T F	80
252	ACAGGGAAAGATAATGGCCTGCATGATTGTGAACCTTTGCTCCACCTGTGATAAAGACCAG	311
81	T G K D N G L H D C E L C S T C D K D Q	100
312	AATATGGTGGCTGACTGTTCTGCCACCAGTGACCGGAAATGCGAGTGCCAAATAGGTCTT	371
101	N M V A D C S A T S D R K C E C Q I G L	120
372	TACTACTATGACCCAAAATTTCCGGAATCATGCCGCCCATGTACCAAGTGTCCCCAAGGA	431
121	Y Y Y D P K F P E S C R P C T K C P Q G	140
432	ATCCCTGTCTCCAGGAATGCAACTCCACAGCTAACACTGTGTGCAGTTCATCTGTTTCA	491
141	I P V L Q E C N S T A N T V C <u>S S S V S</u>	160
492	AATCCCAGAACTGGCTGTTCTACTGATGCTAATTGTCTTCTGTATCTGA	542
161	<u>N P R N W L F L L M L I V F C I *</u>	177
543	AGAAGATAAAGGTTCTACAGATGGTGTCTGTAGCTTCCTTTTATTGCTGTGAAGAGAA	600
601	ACCATGGAGGCAACTCTTTTCATTTTATTTTATTTTAAATGTCTTGAACCTGATTTGAAG	660
661	ACCAGGCTGGACTCAAACCTCACAGAGATCCGGACTAGGCACCTCTAATATAGGAAAACAT	720
721	TGAATTGGGACTGGCTTACAGTTTCAGAAGTTCTGTCCATGATTATCATAGTGCGAAGCA	780
781	TGGAGGCACGGAGGCACACATGGTGTGAGAGAAGAAGCTGAGAGTTCTGCATCTTGATCT	840
841	GCAAGCAATAAAAGGAGACTGTGTGCCACACTACACATAGCTTGAACATAGGAGACCTCA	900
901	AAGCCTGTCCCCACAGTGACAACTTCCTCCAACAAGGTCATACCTCCTAATAATACCAT	960
961	TTCTTATGAGGCAAGCATTCAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCAC	1020
1021	CACAGGTAAACAATTGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCCTTGAGAGTAAGTAA	1080
1081	CAATTTAGATGAAGGCAAGTCTGATCAGGTCCAAAAGAAACTCAGGATGAATGGTCC	1140
1141	ACTGTGGTTCCTATTAACATACTGAAGAACATGACCTCACCTTAGACTTCTCCACCTCAC	1200
1201	TGGCTTCCCTTCCCCTAGCTTCTCATTCAGGTAACCCTGCCATTTTTTGGTAAATGTGC	1260
1261	CTTCTTGGTTCCTCTCCTTTCCCCTCTCTTCTGGTCTTATTTCTCTTCTCTCTCCC	1320
1321	ACTCTCCACCAGCCGCTCTTAAGGCCTGAGTCACTCTGAGGCCATGTTTAACTACTA	1380
1381	CTTTCTCTCTGCTCTGGACTCATCCAGATGTCTCTGGCTGAGCTCTCCCTCCTATCTACA	1440
1441	ATAAAACCTTCCCCCTAACCAGAAATGGAACAGTTTTGTCCTCACTTTGTACATCTGGTG	1500
1501	CCTGAAACC	1509

FIG. 1

7F4 CPDGEY---QSNDVC CKTCPSGIFVKAPCK IPHTQQGQCEKCHPGT FTGKDNGLHDCELC 60  
mTNFR CPGGKYVHSKNNSIC GTKCHKGIYLVSDCP SPGRDTVCRECEKGT FTASQNYLQQCLSGK 60

7F4 IGDKD--QNMVADCS ATSDRKCEC---QIG LYYYDPKFPESGRPC TKCPQGIPLQECNS 120  
mTNFR IGRKEMSQVEISPCQ ADKDTVCGCKENQFQ RYLSETHFQ--CVDC SPGFNGTVTIP-CKE 120

7F4 TANTVC 126  
mTNFR IQNTVC 126

**FIG. 2**

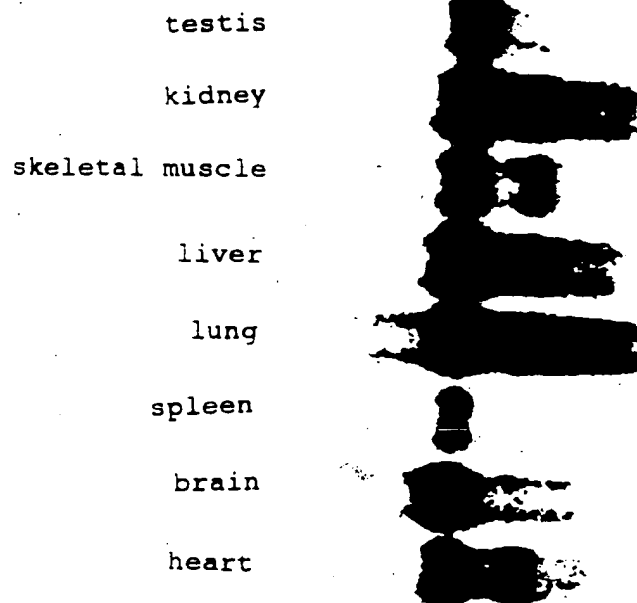


FIG. 3

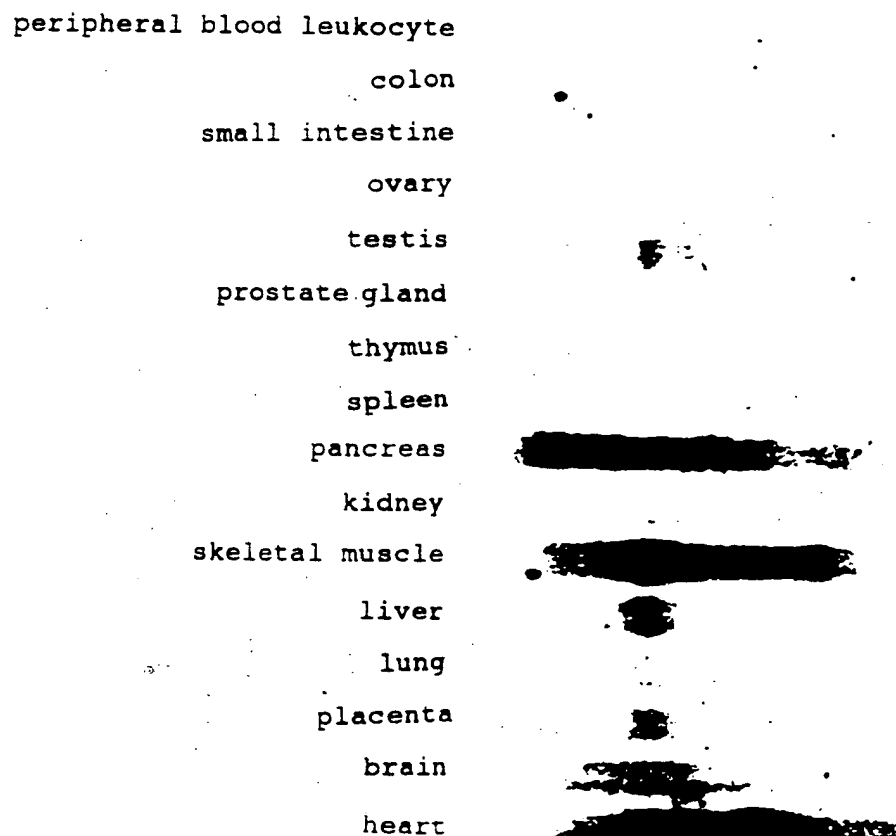
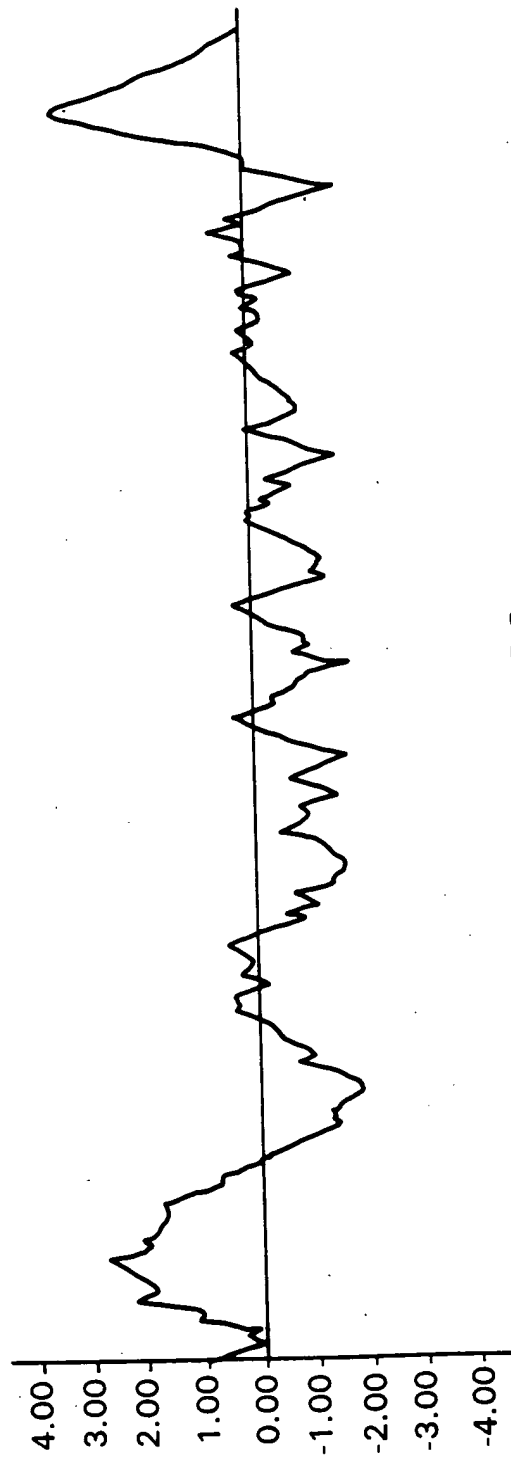
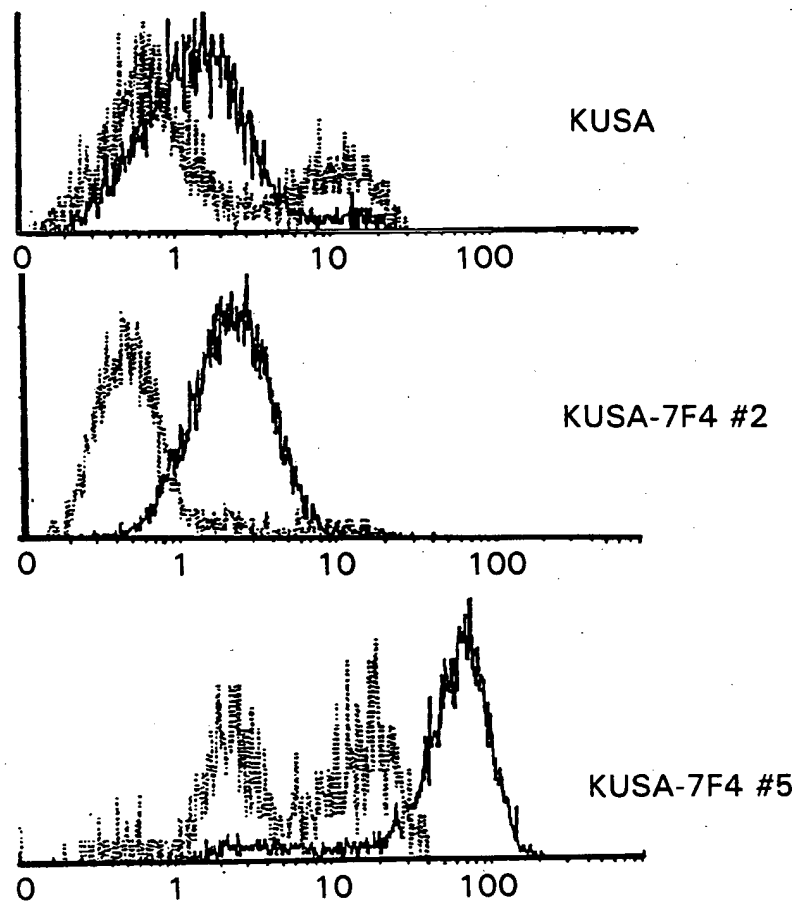


FIG. 4



**FIG. 5A**



**FIG. 5B**

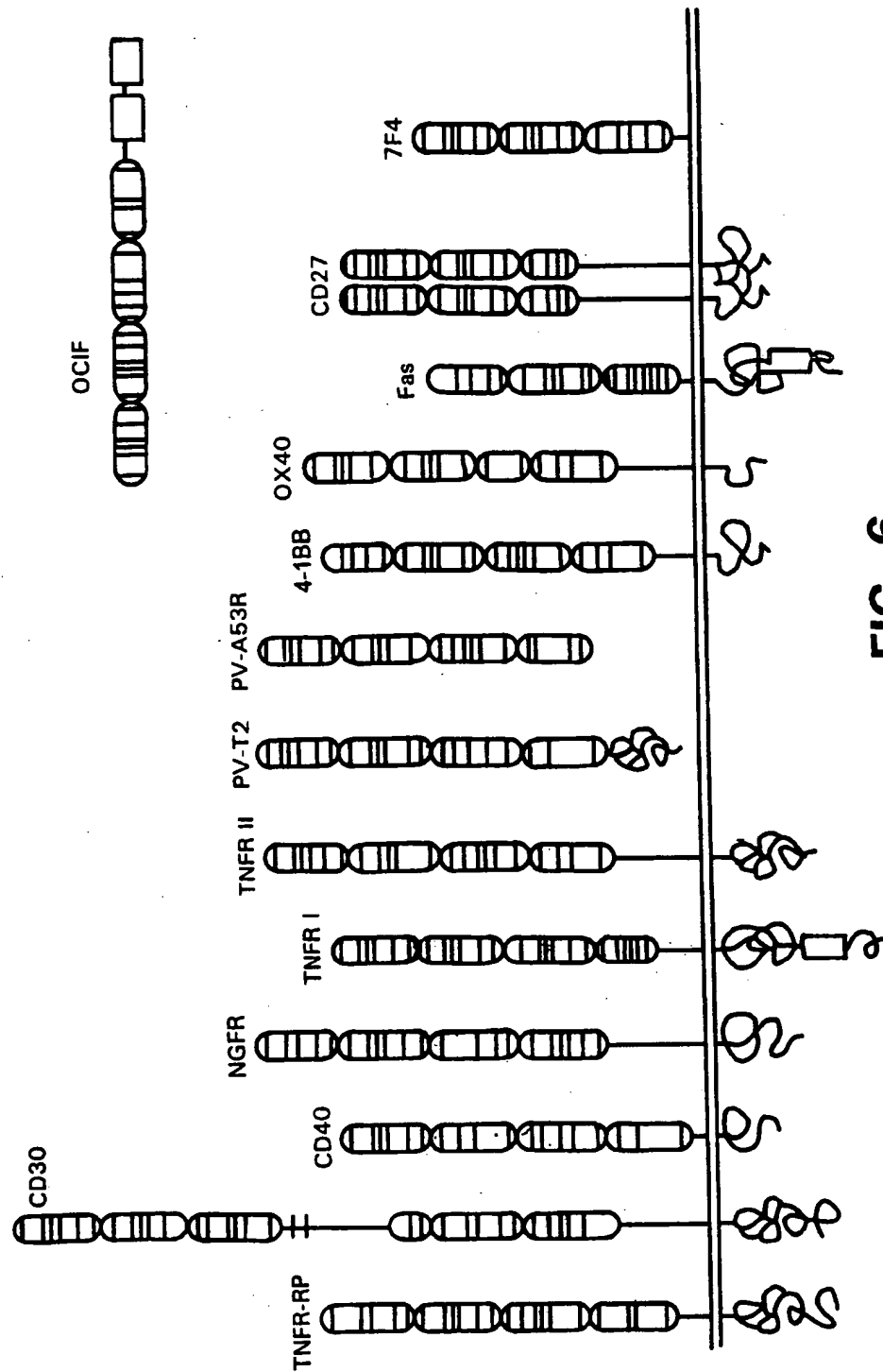


FIG. 6

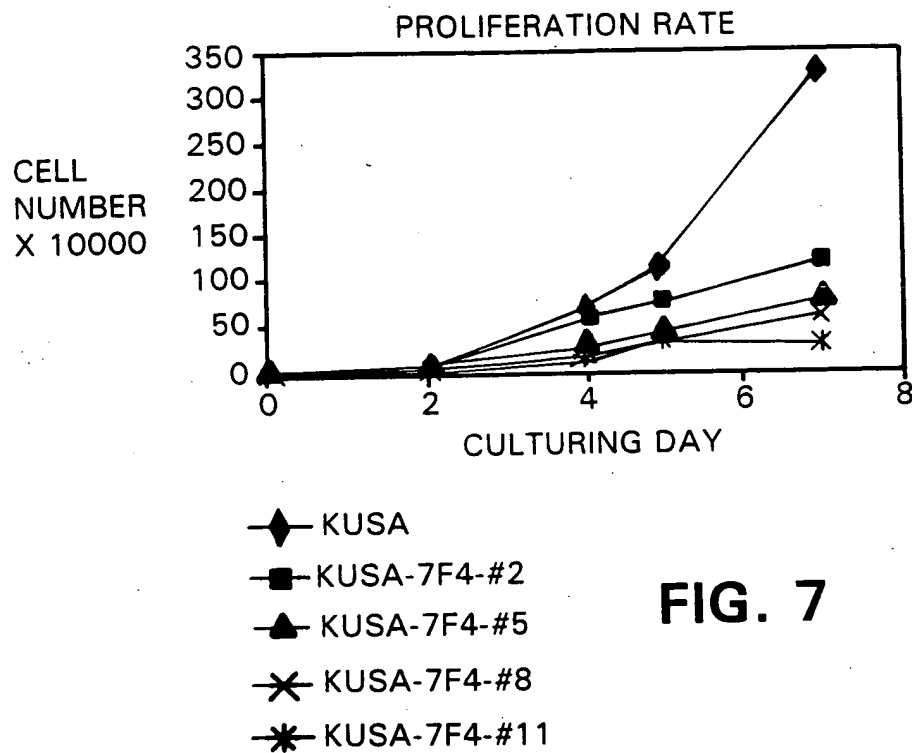


FIG. 7

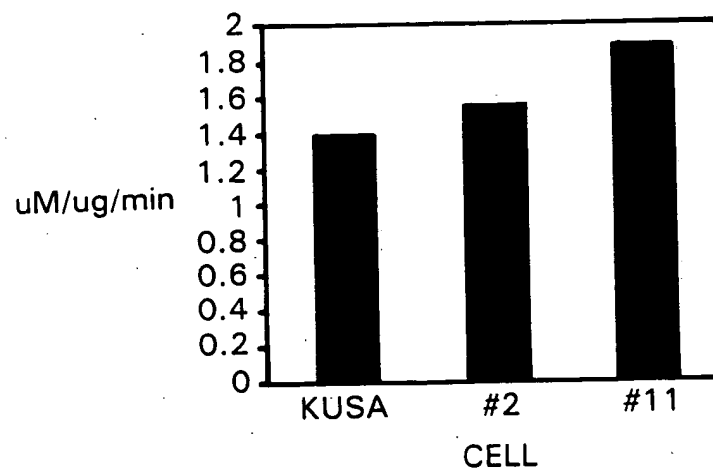
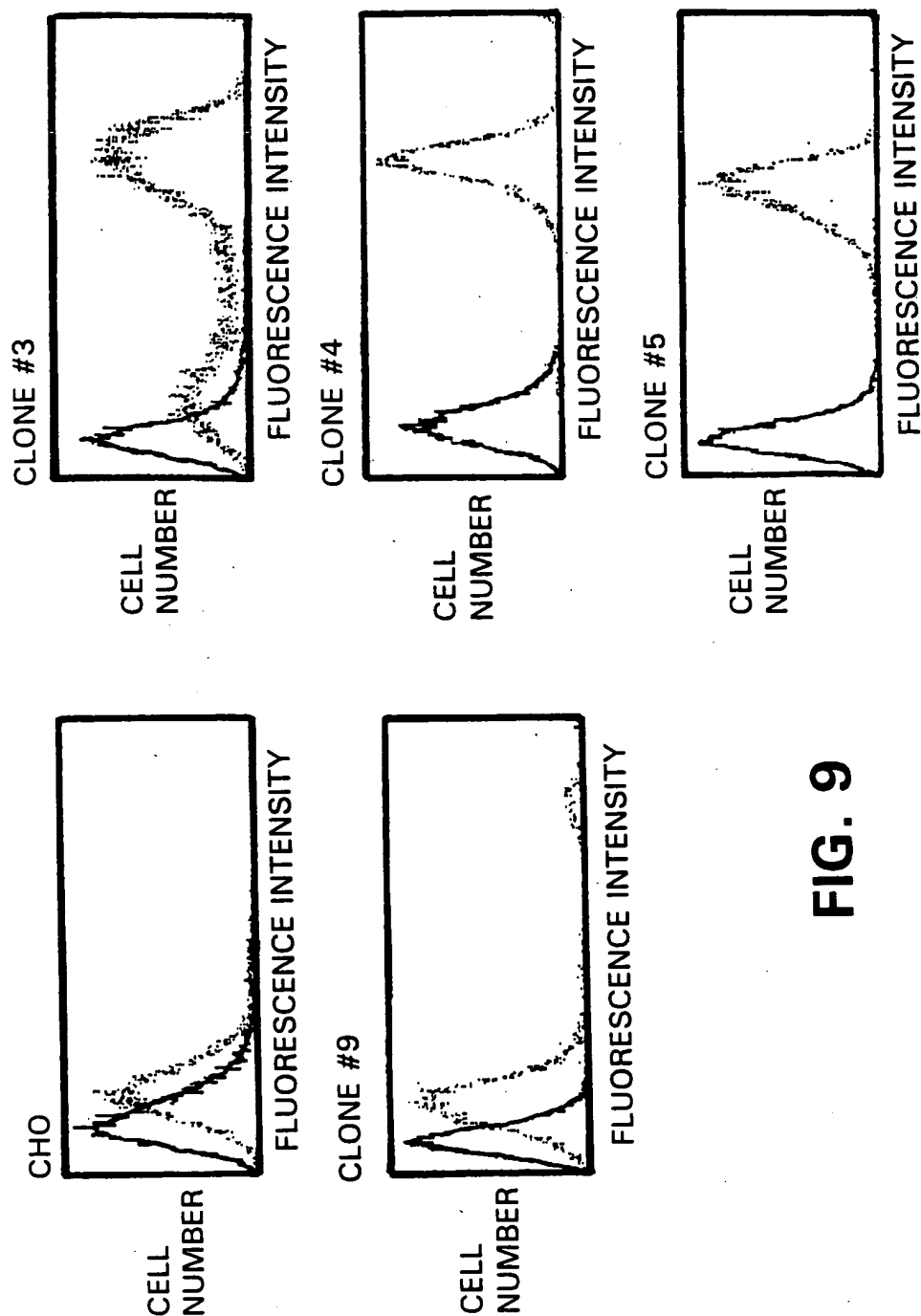
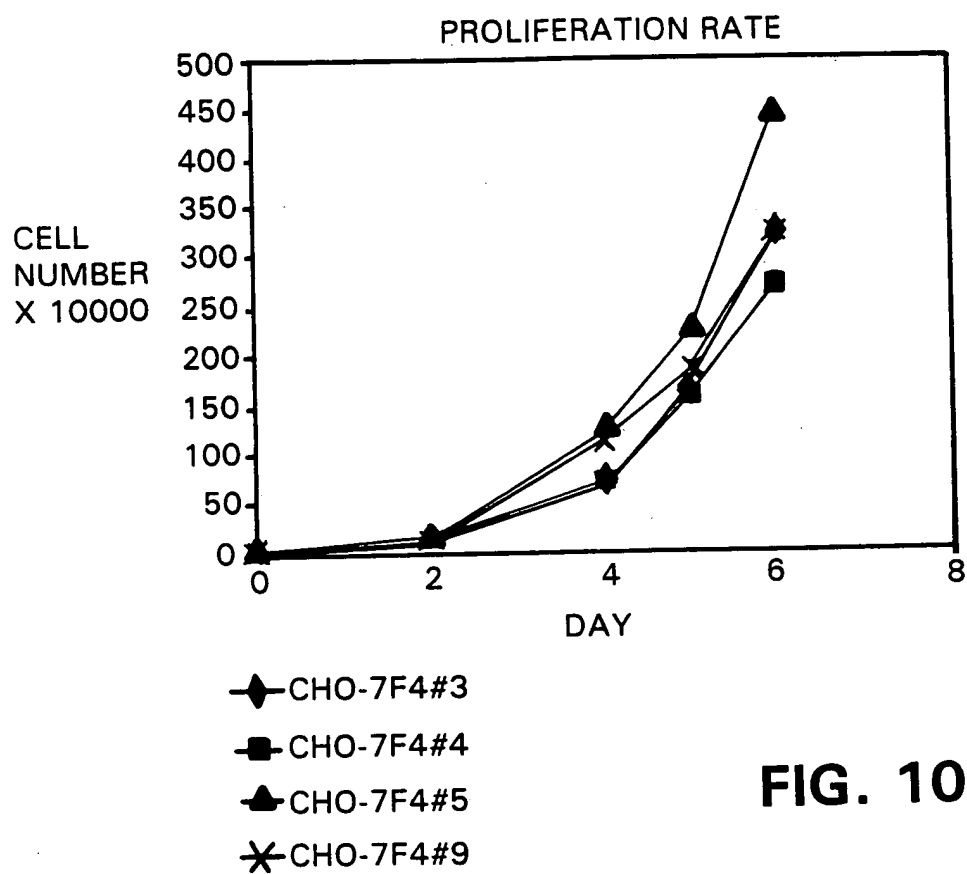


FIG. 8





**FIG. 9**



**FIG. 10**